

FIG. 1A

gtgttgctcc actgtcagtc ctccagagcc tcaagagatc tttgggcat atcagctttc 60
 tttccaaaat gaacacaccc aggggcagga aagaatgctc tttccttggt cattaagggg 120
 cctgggagtc ctggaccagc ttttcatgca gctagaccac ttacatgcaa ctagagcctt 180
 gactttgaaa cgaggggacaa aagcatctct tgctaaaggt aacttctgct gcttagaacc 240
 cagcctcctc accaccatct gatctatctt gttctcttca caaaaggctc tgaagacatc 300
 atg aac cca caa cgg gag gca gca ccc aaa tcc tat gct att cgt gat 348
 Met Asn Pro Gln Arg Glu Ala Ala Pro Lys Ser Tyr Ala Ile Arg Asp
 1 5 10 15
 tct cga cag atg gtg tgg gtc ctg agt gga aat tct tta ata gca gct 396
 Ser Arg Gln Met Val Trp Val Leu Ser Gly Asn Ser Leu Ile Ala Ala
 20 25 30
 cct ctt agc cgc agc att aag cct gtc act ctt cat tta ata gcc tgt 444
 Pro Leu Ser Arg Ser Ile Lys Pro Val Thr Leu His Leu Ile Ala Cys
 35 40 45
 aga gac aca gaa ttc agt gac aag gaa aag ggt aat atg gtt tac ctg 492
 Arg Asp Thr Glu Phe Ser Asp Lys Glu Lys Gly Asn Met Val Tyr Leu
 50 55 60
 gga atc aag gga aaa gat ctc tgt ctc ttc tgt gca gaa att cag ggc 540
 Gly Ile Lys Gly Lys Asp Leu Cys Leu Phe Cys Ala Glu Ile Gln Gly
 65 70 75 80
 aag cct act ttg cag ctt aag gaa aaa aat atc atg gac ctg tat gtg 588
 Lys Pro Thr Leu Gln Leu Lys Glu Lys Asn Ile Met Asp Leu Tyr Val
 85 90 95
 gag aag aaa gca cag aag ccc ttt ctc ttt ttc cac aat aaa gaa ggc 636
 Glu Lys Lys Ala Gln Lys Pro Phe Leu Phe Phe His Asn Lys Glu Gly
 100 105 110
 tcc act tct gtc ttt cag tca gtc tct tac cct ggc tgg ttc ata gcc 684
 Ser Thr Ser Val Phe Gln Ser Val Ser Tyr Pro Gly Trp Phe Ile Ala
 115 120 125
 acc tcc acc aca tca gga cag ccc atc ttt ctc acc aag gag aga ggc 732
 Thr Ser Thr Thr Ser Gly Gln Pro Ile Phe Leu Thr Lys Glu Arg Gly
 130 135 140
 ata act aat aac act aac ttc tac tta gat tct gtg gaa taa 774
 Ile Thr Asn Asn Thr Asn Phe Tyr Leu Asp Ser Val Glu
 145 150 155
 atccagccta ggctgtgggt ggctggttcc aggatagaga atcaagctgt cagagtcac 834
 ttaacagatc attatgcgac tgagttcact agcagttcag cccatccata gcttacctca 894

FIG. 1B

ttcttactat ccaaaagcca cctcctcctc caaacatcca tttctgtacc aagacctca 954
ctcgaatgtc actatcccaa gatgaaacct aaaaatcact ttccattctt tcttgatctt 1014
acccaccat ccactcagct gccatgcca gtttagttaa cccccaaat gctgcttcat 1074
gcaaccttcc attcctattc cttttgcaa cccatgatgt agagatgtgg attcatgaca 1134
ttttgttcat acaacttctt caataaaaca ttataatatg tgcccaaag ataaagctga 1194
agaatgagat gaatgtgaaa ttaaaggttt gcatgtcttc ctaatcctaa 1244

FIG. 2

	1					50
IL-1_delta	-----	-----	-----	MNPQ	REAAPKSYAI	RDSRQMVWVL
IL-1ra-L	-----	-----	-----	MNPQ	REAAPKSYAI	RDSRQMVWVL
IL-1_epsilon	-----	-----	-----	MEKAL	KIDTPQQGSI	QDINHRVWVL
IL-1ra_sec	MEICRGLRSH	LITLLFLFLH	SETICRPSGR	KSSKMQAFRI	WDVNQKTFYL	
IL-1_beta	-----	-----	-----	APVRSLNCTL	RDSQQKSLVM	
consensus	-----	-----	-----	MNPQ	-EAAP-SYAI	RDS-Q-VWVL
	51					100
IL-1_delta	SG.NSLIAAP	LSRSIKPVTI	HLIACRDTEF	SDKEKGNMVY	LGIKGDLC	
IL-1ra-L	SG.NSLIAAP	LSRSIKPVTI	HLIACRDTEF	SDKEKGNMVY	LGIKGDLC	
IL-1_epsilon	QD.QTLIAVP	RKDRMSPVTI	ALISCRHVET	LEKDRGNPIY	LGLNGLNLCL	
IL-1ra_sec	RN.NQLVAGY	LQ...GP.NV	NLEEKIDVVP	IEP...HALF	LGIHGGKMCL	
IL-1_beta	SGPYELKALH	LQGQDMEQQV	.VFSMSFVQG	EESNDKIPVA	LGLKEKNLYL	
consensus	SG-NSLIAAP	L-RSIKPVT-	HLI-CRDVEF	SEKEKGN-VY	LGIKGD-LCL	
	101					150
IL-1_delta	FCAEIQGKPT	LQLKLQGSQD	.NIGKDTCKW	LVGIHTCINL	DVRESCFMG.	
IL-1ra-L	FCAEIQGKPT	LQLKEKNIMD	LYVEKKAQKP	FLFFH...NK	EGSTSVFQSV	
IL-1_epsilon	MCAKVGDOPT	LQLKEKDIMD	LYNQPEPVKS	FLFYH...SQ	SGRNSTFESV	
IL-1ra_sec	SCVKSGDETR	LQLEAVNITD	LSENKQDKR	FAFIR...SD	SGPTTSFESA	
IL-1_beta	SCVLKDDKPT	LQLESVDPKN	.YPKKKMEKR	FVFNKIEINN	KLE...FESA	
consensus	-CA-I-DKPT	LQLKE--IMD	LY--KK--KR	F-FIH--IN-	SGRTS-FES-	
	151					193
IL-1_delta	TLDQWGIGVG	RKKWKSSFQH	HHLRKKDKDF	SSMRTNIGMP	GRM	
IL-1ra-L	SYPGWFIATS	TTSGQPIF..	...LTKERGI	TN.NTNFYLD	SVE	
IL-1_epsilon	AFPGWFIAVS	SEGGCPLILT	QELGKANTTD	FGLTMLF----	---	
IL-1ra_sec	ACPGWFLCTA	MEADQPVSLT	N...MPDEGV	MVTKFYFQED	E--	
IL-1_beta	QFPNWIYSTS	QAENMPVFLG	GTKGGQDITD	FTMQFVSS--	---	
consensus	AFPGWFIATS	-E-GQPVFLT	--LGKKD--D	F-M--NF--D	---	